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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/637,132

DATE: 08/22/2000
 TIME: 08:44:32

ENTERED

Input Set : A:\UCAL-246-02-1US.ST25.txt
 Output Set: N:\CRF3\08212000\I637132.raw

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3 <110> APPLICANT: Baxter, John
4   Fletcher, Robert
5   Kushner, Peter
7 <120> TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
9 <130> FILE REFERENCE: UCAL-246/02/1US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/637,132
12 <141> CURRENT FILING DATE: 2000-08-10
14 <150> PRIOR APPLICATION NUMBER: US 08/980,115
15 <151> PRIOR FILING DATE: 1997-11-26
17 <150> PRIOR APPLICATION NUMBER: US 08/764,870
18 <151> PRIOR FILING DATE: 1996-12-13
20 <150> PRIOR APPLICATION NUMBER: US 60/008,606
21 <151> PRIOR FILING DATE: 1995-12-14
23 <150> PRIOR APPLICATION NUMBER: US 60/008,543
24 <151> PRIOR FILING DATE: 1995-12-13
26 <150> PRIOR APPLICATION NUMBER: US 60/008,540
27 <151> PRIOR FILING DATE: 1995-12-13
29 <160> NUMBER OF SEQ ID NOS: 17
31 <170> SOFTWARE: PatentIn version 3.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 410
35 <212> TYPE: PRT
36 <213> ORGANISM: Rattus sp.
38 <220> FEATURE:
39 <221> NAME/KEY: DOMAIN
40 <222> LOCATION: (157)..(410)
41 <223> OTHER INFORMATION: minimal ligand binding domain
44 <220> FEATURE:
45 <221> NAME/KEY: DOMAIN
46 <222> LOCATION: (393)..(405)
47 <223> OTHER INFORMATION: activation domain
50 <400> SEQUENCE: 1
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53 1 5 10 15
55 Asn Ser Ala Arg Ser Pro Asp Gly Lys Arg Lys Arg Lys Asn Gly Gln
56 20 25 30
58 Cys Pro Leu Lys Ser Ser Met Ser Gly Tyr Ile Pro Ser Tyr Leu Asp
59 35 40 45
61 Lys Asp Glu Gln Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His
62 50 55 60
64 Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr
65 65 70 75 80
67 Ile Gln Lys Asn Leu His Pro Thr Tyr Ser Cys Lys Tyr Asp Ser Cys
68 85 90 95
70 Cys Val Ile Asp Lys Ile Thr Arg Asn Gln Cys Gln Leu Cys Arg Phe
71 100 105 110
73 Lys Lys Cys Ile Ala Val Gly Met Ala Met Asp Leu Val Leu Asp Asp

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74          115          120          125
76 Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Gln Asn Arg Glu Arg
77          130          135          140
79 Arg Arg Lys Glu Glu Met Ile Arg Ser Leu Gln Gln Arg Pro Glu Pro
80 145          150          155          160
82 Thr Pro Glu Glu Trp Asp Leu Ile His Val Ala Thr Glu Ala His Arg
83          165          170          175
85 Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg Lys Phe Leu
86          180          185          190
88 Pro Asp Asp Ile Gly Gln Ser Pro Ile Val Ser Met Pro Asp Gly Asp
89          195          200          205
91 Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile Ile Thr Pro
92          210          215          220
94 Ala Ile Thr Arg Val Val Asp Phe Ala Lys Lys Leu Pro Met Phe Ser
95 225          230          235          240
97 Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly Cys Cys Met
98          245          250          255
100 Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro Glu Ser Asp
101          260          265          270
103 Thr Leu Thr Leu Ser Gly Glu Met Thr Val Lys Arg Lys Gln Leu Lys
104          275          280          285
106 Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Glu Leu Gly Lys
107          290          295          300
109 Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala Leu Leu Gln
110 305          310          315          320
112 Ala Val Leu Leu Met Ser Thr Asp Arg Ser Gly Leu Leu Cys Val Asp
113          325          330          335
115 Lys Ile Glu Lys Ser Gln Glu Ala Tyr Leu Leu Ala Phe Glu His Tyr
116          340          345          350
118 Val Asn His Arg Lys His Asn Ile Pro His Phe Trp Pro Lys Leu Leu
119          355          360          365
121 Met Lys Val Thr Asp Leu Arg Met Ile Gly Ala Cys His Ala Ser Arg
122          370          375          380
124 Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Phe Pro Pro Leu
125 385          390          395          400
127 Phe Leu Glu Val Phe Glu Asp Gln Glu Val
128          405          410
130 <210> SEQ ID NO: 2
131 <211> LENGTH: 410
132 <212> TYPE: PRT
133 <213> ORGANISM: Homo sapiens
135 <220> FEATURE:
136 <221> NAME/KEY: DOMAIN
137 <222> LOCATION: (157)..(410)
138 <223> OTHER INFORMATION: minimal ligand binding domain
141 <400> SEQUENCE: 2
143 Met Glu Gln Lys Pro Ser Lys Val Glu Cys Gly Ser Asp Pro Glu Glu
144 1          5          10          15
146 Asn Ser Ala Arg Ser Pro Asp Gly Lys Arg Lys Arg Lys Asn Gly Gln

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147          20          25          30
149 Cys Ser Leu Lys Thr Ser Met Ser Gly Tyr Ile Pro Ser Tyr Leu Asp
150          35          40          45
152 Lys Asp Glu Gln Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His
153          50          55          60
155 Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr
156 65          70          75          80
158 Ile Gln Lys Asn Leu His Pro Thr Tyr Ser Cys Lys Tyr Asp Ser Cys
159          85          90          95
161 Cys Val Ile Asp Lys Ile Thr Arg Asn Gln Cys Gln Leu Cys Arg Phe
162          100          105          110
164 Lys Lys Cys Ile Ala Val Gly Met Ala Met Asp Leu Val Leu Asp Asp
165          115          120          125
167 Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Gln Asn Arg Glu Arg
168          130          135          140
170 Arg Arg Lys Glu Glu Met Ile Arg Ser Leu Gln Gln Arg Pro Glu Pro
171 145          150          155          160
173 Thr Pro Glu Glu Trp Asp Leu Ile His Ile Ala Thr Glu Ala His Arg
174          165          170          175
176 Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg Lys Phe Leu
177          180          185          190
179 Pro Asp Asp Ile Gly Gln Ser Pro Ile Val Ser Met Pro Asp Gly Asp
180          195          200          205
182 Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile Ile Thr Pro
183          210          215          220
185 Ala Ile Thr Arg Val Val Asp Phe Ala Lys Lys Leu Pro Met Phe Ser
186 225          230          235          240
188 Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly Cys Cys Met
189          245          250          255
191 Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro Glu Ser Asp
192          260          265          270
194 Thr Leu Thr Leu Ser Gly Glu Met Ala Val Lys Arg Glu Gln Leu Lys
195          275          280          285
197 Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Glu Leu Gly Lys
198          290          295          300
200 Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala Leu Leu Gln
201 305          310          315          320
203 Ala Val Leu Leu Met Ser Thr Asp Arg Ser Gly Leu Leu Cys Val Asp
204          325          330          335
206 Lys Ile Glu Lys Ser Gln Glu Ala Tyr Leu Leu Ala Phe Glu His Tyr
207          340          345          350
209 Val Asn His Arg Lys His Asn Ile Pro His Phe Trp Pro Lys Leu Leu
210          355          360          365
212 Met Lys Val Thr Asp Leu Arg Met Ile Gly Ala Cys His Ala Ser Arg
213          370          375          380
215 Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Phe Pro Pro Leu
216 385          390          395          400
218 Phe Leu Glu Val Phe Glu Asp Gln Glu Val
219          405          410

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221 <210> SEQ ID NO: 3
222 <211> LENGTH: 461
223 <212> TYPE: PRT
224 <213> ORGANISM: Homo sapiens
226 <220> FEATURE:
227 <221> NAME/KEY: DOMAIN
228 <222> LOCATION: (211)..(461)
229 <223> OTHER INFORMATION: minimal ligand binding domain
232 <400> SEQUENCE: 3
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235 1 5 10 15
237 Pro Lys His Cys Pro Asp Arg Glu His Asp Trp Lys Leu Val Gly Met
238 20 25 30
240 Ser Glu Ala Cys Leu His Arg Lys Ser His Ser Glu Arg Arg Ser Thr
241 35 40 45
243 Leu Lys Asn Glu Gln Ser Ser Pro His Leu Ile Gln Thr Thr Trp Thr
244 50 55 60
246 Ser Ser Ile Phe His Leu Asp His Asp Asp Val Asn Asp Gln Ser Val
247 65 70 75 80
249 Ser Ser Ala Gln Thr Phe Gln Thr Glu Glu Lys Lys Cys Lys Gly Tyr
250 85 90 95
252 Ile Pro Ser Tyr Leu Asp Lys Asp Glu Leu Cys Val Val Cys Gly Asp
253 100 105 110
255 Lys Ala Thr Gly Tyr His Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys
256 115 120 125
258 Gly Phe Phe Arg Arg Thr Ile Gln Lys Asn Leu His Pro Ser Tyr Ser
259 130 135 140
261 Cys Lys Tyr Glu Gly Lys Cys Val Ile Asp Lys Val Thr Arg Asn Gln
262 145 150 155 160
264 Cys Gln Glu Cys Arg Phe Lys Lys Cys Ile Tyr Val Gly Met Ala Thr
265 165 170 175
267 Asp Leu Val Leu Asp Asp Ser Lys Arg Leu Ala Lys Arg Lys Leu Ile
268 180 185 190
270 Glu Glu Asn Arg Glu Lys Arg Arg Arg Glu Glu Leu Gln Lys Ser Ile
271 195 200 205
273 Gly His Lys Pro Glu Pro Thr Asp Glu Glu Trp Glu Leu Ile Lys Thr
274 210 215 220
276 Val Thr Glu Ala His Val Ala Thr Asn Ala Gln Gly Ser His Trp Lys
277 225 230 235 240
279 Gln Lys Pro Lys Phe Leu Pro Glu Asp Ile Gly Gln Ala Pro Ile Val
280 245 250 255
282 Asn Ala Pro Glu Gly Gly Lys Val Asp Leu Glu Ala Phe Ser His Phe
283 260 265 270
285 Thr Lys Ile Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys
286 275 280 285
288 Lys Leu Pro Met Phe Cys Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu
289 290 295 300
291 Leu Lys Gly Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg
292 305 310 315 320

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294 Tyr Asp Pro Glu Ser Glu Thr Leu Thr Leu Asn Gly Glu Met Ala Val
295                               325          330          335
297 Ile Arg Gly Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala
298                               340          345          350
300 Ile Phe Asp Leu Gly Met Ser Leu Ser Ser Phe Asn Leu Asp Asp Thr
301                               355          360          365
303 Glu Val Ala Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Pro
304                               370          375          380
306 Gly Leu Ala Cys Val Glu Arg Ile Glu Lys Tyr Gln Asp Ser Phe Leu
307 385                               390          395          400
309 Leu Ala Phe Glu His Tyr Ile Asn Tyr Arg Lys His His Val Thr His
310                               405          410          415
312 Phe Trp Pro Lys Leu Leu Met Lys Val Thr Asp Leu Arg Met Ile Gly
313                               420          425          430
315 Ala Cys His Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr
316                               435          440          445
318 Glu Leu Leu Pro Pro Leu Phe Leu Glu Val Phe Glu Asp
319                               450          455          460
321 <210> SEQ ID NO: 4
322 <211> LENGTH: 416
323 <212> TYPE: PRT
324 <213> ORGANISM: Homo sapiens
326 <220> FEATURE:
327 <221> NAME/KEY: DOMAIN
328 <222> LOCATION: (131)..(373)
329 <223> OTHER INFORMATION: minimal ligand binding domain
332 <400> SEQUENCE: 4
334 Pro Asn Ser Asn His Val Ala Ser Gly Ala Gly Glu Ala Ala Ile Glu
335 1                               5          10          15
337 Thr Gln Ser Ser Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro
338                               20          25          30
340 Pro Pro Leu Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys
341                               35          40          45
343 Ser Ser Gly Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly
344 50                               55          60          65
346 Phe Phe Arg Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg
347 65                               70          75          80
349 Asp Lys Asn Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr
350                               85          90          95
352 Cys Arg Leu Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val
353                               100         105         110
355 Arg Asn Asp Arg Asn Lys Lys Lys Lys Glu Val Pro Lys Pro Glu Cys
356                               115         120         125
358 Ser Glu Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys
359                               130         135         140
361 Val Arg Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys Gln Leu Gly
362 145                               150         155         160
364 Lys Tyr Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser Leu Asp Ile
365                               165         170         175

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VERIFICATION SUMMARY

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DATE: 08/22/2000

TIME: 08:44:33

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number